

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Kenneth A. Jones
Thomas M. Laz
Beth Borowsky

(ii) TITLE OF INVENTION: DNA Encoding a GABABR2 Polypeptide And
Uses Thereof

(iii) NUMBER OF SEQUENCES: 55

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/211,755
(B) FILING DATE: 15-Dec-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: White Esq., John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 54002-D/JPW

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 212-278-0400
(B) TELEFAX: 212-391-0525

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGACCTCGGG GCAGGTCCTG GTGCAGAGCG TCGCCAAGGA CGCCGAGAGG GAGGCGGGAT 60
TGCCCAGACA TCCTTCAGCG AAGTGCATGT GTGTTTGTAA ACCATCGTTG GCTGTCGGGA 120

GACCGCGAGG	ACCGGTCCAG	GCTGCGGCGG	AGTCGAGGGC	GAGGGAGAGG	CCGCGTGAGT	180
GAGCAGAGTC	CAGAGCCGTG	CGCCCCCAGA	ACTGCGCGTC	CGCCCCGTGC	ACCCCCGCGC	240
GCCATGCCCCA	GTTGCCCCGC	GCGCTCTGCT	ACGGGCCCCG	TCTCCATCAT	GGGCCTCATG	300
CCGCTCACCA	AGGAGGTGGC	CAAGGGCAGC	ATCGGGCGCG	GTGTGCTCCC	CGCCGTGGAA	360
CTGGCCATCG	AGCAGATCCG	CAACGAGTCA	CTCCTGCGCC	CCTACTTCCT	CGACCTGCGG	420
CTCTATGACA	CGGAGTGCGA	CAACGCAAAA	GGGTTGAAAG	CCTTCTACGA	TGCGATAAAA	480
TACGGGCCGA	ACCACTTGAT	GGTGTTTGGA	GGCGTCTGTC	CATCCGTCAC	ATCCATCATT	540
GCAGAGTCCC	TCCAAGGCTG	GAATCTGGTG	CAGCTTTCTT	TTGCTGCAAC	CACGCCTGTT	600
CTAGCCGATA	AGAAAAAATA	CCCTTATTTT	TTTCGGACCG	TCCCATCAGA	CAATGCGGTG	660
AATCCAGCCA	TTCTGAAGTT	GCTCAAGCAC	TACCAGTGGA	AGCGCGTGGG	CACGCTGACG	720
CAAGACGTTT	AGAGGTTCTC	TGAGGTGCGG	AATGACCTGA	CTGGAGTTCT	GTATGGCGAG	780
GACATTGAGA	TTTCAGACAC	CGAGAGCTTC	TCCAACGATC	CCTGTACCAG	TGTCAAAAAG	840
CTGAAGGGGA	ATGATGTGCG	GATCATCCTT	GGCCAGTTTG	ACCAGAATAT	GGCAGCAAAA	900
GTGTTCTGTT	GTGCATACGA	GGAGAACATG	TATGGTAGTA	AATATCAGTG	GATCATTCCG	960
GGCTGGTACG	AGCCTTCTTG	GTGGGAGCAG	GTGCACACGG	AAGCCAACTC	ATCCCGCTGC	1020
CTCCGGAAGA	ATCTGCTTGC	TGCCATGGAG	GGCTACATTG	GCGTGGATTT	CGAGCCCCTG	1080
AGCTCCAAGC	AGATCAAGAC	CATCTCAGGA	AAGACTCCAC	AGCAGTATGA	GAGAGAGTAC	1140
AACAACAAGC	GGTCAGGCGT	GGGGCCAGC	AAGTTCCACG	GGTACGCCTA	CGATGGGCATC	1200
TGGGTCATCG	CCAAGACACT	GCAGAGGGCC	ATGGAGACAC	TGCATGCCAG	CAGCCGGCAC	1260
CAGCGGATCC	AGGACTTCAA	CTACACGGAC	CACACGCTGG	GCAGGATCAT	CCTCAATGCC	1320
ATGAACGAGA	CCAACTTCTT	CGGGGTCACG	GGTCAAGTTG	TATTCCGGAA	TGGGGAGAGA	1380
ATGGGGACCA	TTAAATTTAC	TCAATTTCAA	GACAGCAGGG	AGGTGAAGGT	GGGAGAGTAC	1440
AACGCTGTGG	CCGACACACT	GGAGATCATC	AATGACACCA	TCAGGTTCCA	AGGATCCGAA	1500
CCACCAAAAAG	ACAAGACCAT	CATCCTGGAG	CAGCTGCGGA	AGATCTCCCT	ACCTCTCTAC	1560
AGCATCCTCT	CTGCCCTCAC	CATCCTCGGG	ATGATCATGG	CCAGTGCTTT	TCTCTTCTTC	1620
AACATCAAGA	ACCGGAATCA	GAAGCTCATA	AAGATGTCGA	GTCCATACAT	GAACAACCTT	1680
ATCATCCTTG	GAGGGATGCT	TTCCTATGCT	TCCATATTTT	TCTTTGGCCT	TGATGGATCC	1740
TTTGTCTCTG	AAAAGACCTT	TGAAACACTT	TGCACCGTCA	GGACCTGGAT	TCTCACCGTG	1800
GGCTACACGA	CCGCTTTTGG	GGCCATGTTT	GCAAAGACCT	GGAGAGTCCA	CGCCATCTTC	1860
AAAAATGTGA	AAATGAAGAA	GAAGATCATC	AAGGACCAGA	AACTGCTTGT	GATCGTGGGG	1920
GGCATGCTGC	TGATCGACCT	GTGTATCCTG	ATCTGCTGGC	AGGCTGTGGA	CCCCCTGCGA	1980
AGGACAGTGG	AGAAGTACAG	CATGGAGCCG	GACCCAGCAG	GACGGGATAT	CTCCATCCGC	2040

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CCTCTCCTGG AGCACTGTGA GAACACCCAT ATGACCATCT GGCTTGGCAT CGTCTATGCC 2100
TACAAGGGAC TTCTCATGTT GTTCGGTTGT TTCTTAGCTT GGGAGACCCG CAACGTCAGC 2160
ATCCCCGCAC TCAACGACAG CAAGTACATC GGGATGAGTG TCTACAACGT GGGGATCATG 2220
TGCATCATCG GGGCCGCTGT CTCCTTCCTG ACCCGGGACC AGCCCAATGT GCAGTTCTGC 2280
ATCGTGGCTC TGGTCATCAT CTTCTGCAGC ACCATCACCC TCTGCCTGGT ATTCTGTCGG 2340
AAGCTCATCA CCCTGAGAAC AAACCCAGAT GCAGCAACGC AGAACAGGCG ATTCCAGTTC 2400
ACTCAGAATC AGAAGAAAGA AGATTCTAAA ACGTCCACCT CGGTCACCAG TGTGAACCAA 2460
GCCAGCACAT CCCGCCTGGA GGGCCTACAG TCAGAAAACC ATCGCCTGCG AATGAAGATC 2520
ACAGAGCTGG ATAAAGACTT GGAAGAGGTC ACCATGCAGC TGCAGGACAC ACCAGAAAAG 2580
ACCACCTACA TTAAACAGAA CCACTACCAA GAGCTCAATG ACATCCTCAA CCTGGGAAAC 2640
TTCCTGAGA GCACAGATGG AGGAAAGGCC ATTTTAAAAA ATCACCTCGA TCAAAATCCC 2700
CAGCTACAGT GGAACACAAC AGAGCCCTCT CGAACATGCA AAGATCCTAT AGAAGATATA 2760
AACTCTCCAG AACACATCCA GCGTCGGCTG TCCCTCCAGC TCCCCATCCT CCACCACGCC 2820
TACCTCCCAT CCATCGGAGG CGTGGACGCC AGCTGTGTCA GCCCCTGCGT CAGCCCCACC 2880
GCCAGCCCCC GCCACAGACA TGTGCCACCC TCCTTCCGAG TCATGGTCTC GGGCCTGTAA 2940
GGGTGGGAGG CCTGGGCCCC GGGCCTCCCC CGTGACAGAA CCACACTGGG CAGAGGGGTC 3000
TGCTGCAGAA AACTGTTCGG CTCTGGCTGC GGAGAAGCTG GGCACCATGG CTGGCCTCTC 3060
AGGACCACTC GGATGGCACT CAGGTGGACA GGACGGGGCA GGGGGAGACT TGGCACCTGA 3120
CCTCGAGCCT TATTTGTGAA GTCCTTATTT CTTCAAAAG AAGAGGAACG GAAATGGGAC 3180
GTCTTCCTTA ACATCTGCAA ACAAGGAGGC GCTGGGATAT CAAACTTGCA AAAAAAAAAA 3240
AAAA

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 898 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Pro Ser Cys Pro Ala Arg Ser Ala Thr Gly Pro Leu Ser Ile Met
1           5           10          15

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Gly Leu Met Pro Leu Thr Lys Glu Val Ala Lys Gly Ser Ile Gly Arg

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140

20					25					30					
Gly	Val	Leu	Pro	Ala	Val	Glu	Leu	Ala	Ile	Glu	Gln	Ile	Arg	Asn	Glu
	35					40						45			
Ser	Leu	Leu	Arg	Pro	Tyr	Phe	Leu	Asp	Leu	Arg	Leu	Tyr	Asp	Thr	Glu
	50					55					60				
Cys	Asp	Asn	Ala	Lys	Gly	Leu	Lys	Ala	Phe	Tyr	Asp	Ala	Ile	Lys	Tyr
	65					70					75				80
Gly	Pro	Asn	His	Leu	Met	Val	Phe	Gly	Gly	Val	Cys	Pro	Ser	Val	Thr
				85					90					95	
Ser	Ile	Ile	Ala	Glu	Ser	Leu	Gln	Gly	Trp	Asn	Leu	Val	Gln	Leu	Ser
			100					105					110		
Phe	Ala	Ala	Thr	Thr	Pro	Val	Leu	Ala	Asp	Lys	Lys	Lys	Tyr	Pro	Tyr
			115				120						125		
Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Asn	Ala	Val	Asn	Pro	Ala	Ile	Leu
	130					135					140				
Lys	Leu	Leu	Lys	His	Tyr	Gln	Trp	Lys	Arg	Val	Gly	Thr	Leu	Thr	Gln
	145					150					155				160
Asp	Val	Gln	Arg	Phe	Ser	Glu	Val	Arg	Asn	Asp	Leu	Thr	Gly	Val	Leu
				165					170					175	
Tyr	Gly	Glu	Asp	Ile	Glu	Ile	Ser	Asp	Thr	Glu	Ser	Phe	Ser	Asn	Asp
			180					185						190	
Pro	Cys	Thr	Ser	Val	Lys	Lys	Leu	Lys	Gly	Asn	Asp	Val	Arg	Ile	Ile
			195				200					205			
Leu	Gly	Gln	Phe	Asp	Gln	Asn	Met	Ala	Ala	Lys	Val	Phe	Cys	Cys	Ala
	210					215					220				
Tyr	Glu	Glu	Asn	Met	Tyr	Gly	Ser	Lys	Tyr	Gln	Trp	Ile	Ile	Pro	Gly
	225					230					235				240
Trp	Tyr	Glu	Pro	Ser	Trp	Trp	Glu	Gln	Val	His	Thr	Glu	Ala	Asn	Ser
				245					250					255	
Ser	Arg	Cys	Leu	Arg	Lys	Asn	Leu	Leu	Ala	Ala	Met	Glu	Gly	Tyr	Ile
			260					265					270		
Gly	Val	Asp	Phe	Glu	Pro	Leu	Ser	Ser	Lys	Gln	Ile	Lys	Thr	Ile	Ser
		275					280					285			
Gly	Lys	Thr	Pro	Gln	Gln	Tyr	Glu	Arg	Glu	Tyr	Asn	Asn	Lys	Arg	Ser
	290					295					300				
Gly	Val	Gly	Pro	Ser	Lys	Phe	His	Gly	Tyr	Ala	Tyr	Asp	Gly	Ile	Trp
	305					310					315				320
Val	Ile	Ala	Lys	Thr	Leu	Gln	Arg	Ala	Met	Glu	Thr	Leu	His	Ala	Ser
				325					330					335	
Ser	Arg	His	Gln	Arg	Ile	Gln	Asp	Phe	Asn	Tyr	Thr	Asp	His	Thr	Leu
			340					345					350		
Gly	Arg	Ile	Ile	Leu	Asn	Ala	Met	Asn	Glu	Thr	Asn	Phe	Phe	Gly	Val

	355		360		365										
Thr	Gly	Gln	Val	Val	Phe	Arg	Asn	Gly	Glu	Arg	Met	Gly	Thr	Ile	Lys
	370					375					380				
Phe	Thr	Gln	Phe	Gln	Asp	Ser	Arg	Glu	Val	Lys	Val	Gly	Glu	Tyr	Asn
385					390					395					400
Ala	Val	Ala	Asp	Thr	Leu	Glu	Ile	Ile	Asn	Asp	Thr	Ile	Arg	Phe	Gln
				405					410					415	
Gly	Ser	Glu	Pro	Pro	Lys	Asp	Lys	Thr	Ile	Ile	Leu	Glu	Gln	Leu	Arg
			420					425					430		
Lys	Ile	Ser	Leu	Pro	Leu	Tyr	Ser	Ile	Leu	Ser	Ala	Leu	Thr	Ile	Leu
		435					440					445			
Gly	Met	Ile	Met	Ala	Ser	Ala	Phe	Leu	Phe	Phe	Asn	Ile	Lys	Asn	Arg
	450					455					460				
Asn	Gln	Lys	Leu	Ile	Lys	Met	Ser	Ser	Pro	Tyr	Met	Asn	Asn	Leu	Ile
465					470					475					480
Ile	Leu	Gly	Gly	Met	Leu	Ser	Tyr	Ala	Ser	Ile	Phe	Leu	Phe	Gly	Leu
				485					490					495	
Asp	Gly	Ser	Phe	Val	Ser	Glu	Lys	Thr	Phe	Glu	Thr	Leu	Cys	Thr	Val
			500					505					510		
Arg	Thr	Trp	Ile	Leu	Thr	Val	Gly	Tyr	Thr	Thr	Ala	Phe	Gly	Ala	Met
		515					520					525			
Phe	Ala	Lys	Thr	Trp	Arg	Val	His	Ala	Ile	Phe	Lys	Asn	Val	Lys	Met
	530					535					540				
Lys	Lys	Lys	Ile	Ile	Lys	Asp	Gln	Lys	Leu	Leu	Val	Ile	Val	Gly	Gly
545					550					555					560
Met	Leu	Leu	Ile	Asp	Leu	Cys	Ile	Leu	Ile	Cys	Trp	Gln	Ala	Val	Asp
				565				570						575	
Pro	Leu	Arg	Arg	Thr	Val	Glu	Lys	Tyr	Ser	Met	Glu	Pro	Asp	Pro	Ala
			580					585					590		
Gly	Arg	Asp	Ile	Ser	Ile	Arg	Pro	Leu	Leu	Glu	His	Cys	Glu	Asn	Thr
		595					600					605			
His	Met	Thr	Ile	Trp	Leu	Gly	Ile	Val	Tyr	Ala	Tyr	Lys	Gly	Leu	Leu
	610					615					620				
Met	Leu	Phe	Gly	Cys	Phe	Leu	Ala	Trp	Glu	Thr	Arg	Asn	Val	Ser	Ile
625					630					635					640
Pro	Ala	Leu	Asn	Asp	Ser	Lys	Tyr	Ile	Gly	Met	Ser	Val	Tyr	Asn	Val
				645					650					655	
Gly	Ile	Met	Cys	Ile	Ile	Gly	Ala	Ala	Val	Ser	Phe	Leu	Thr	Arg	Asp
			660					665					670		
Gln	Pro	Asn	Val	Gln	Phe	Cys	Ile	Val	Ala	Leu	Val	Ile	Ile	Phe	Cys
		675					680					685			
Ser	Thr	Ile	Thr	Leu	Cys	Leu	Val	Phe	Val	Pro	Lys	Leu	Ile	Thr	Leu

1690	695	700
Arg Thr Asn Pro Asp	Ala Ala Thr Gln Asn	Arg Arg Phe Gln Phe Thr
705	710	715 720
Gln Asn Gln Lys Lys	Glu Asp Ser Lys Thr	Ser Thr Ser Val Thr Ser
	725	730 735
Val Asn Gln Ala Ser Thr Ser Arg	Leu Glu Gly Leu Gln Ser Glu Asn	
	740	745 750
His Arg Leu Arg Met Lys Ile Thr Glu Leu Asp Lys Asp Leu Glu Glu		
	755	760 765
Val Thr Met Gln Leu Gln Asp Thr Pro Glu Lys Thr Thr Tyr Ile Lys		
	770	775 780
Gln Asn His Tyr Gln Glu Leu Asn Asp Ile Leu Asn Leu Gly Asn Phe		
785	790	795 800
Thr Glu Ser Thr Asp Gly Gly Lys Ala Ile Leu Lys Asn His Leu Asp		
	805	810 815
Gln Asn Pro Gln Leu Gln Trp Asn Thr Thr Glu Pro Ser Arg Thr Cys		
	820	825 830
Lys Asp Pro Ile Glu Asp Ile Asn Ser Pro Glu His Ile Gln Arg Arg		
	835	840 845
Leu Ser Leu Gln Leu Pro Ile Leu His His Ala Tyr Leu Pro Ser Ile		
	850	855 860
Gly Gly Val Asp Ala Ser Cys Val Ser Pro Cys Val Ser Pro Thr Ala		
865	870	875 880
Ser Pro Arg His Arg His Val Pro Pro Ser Phe Arg Val Met Val Ser		
	885	890 895
Gly Leu		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGCTTCCC CGCCGAGCTC CGGGCAGCCC CGGCCGCCGC CGCCGCCGCC GCCGCCCCGC	60
CGCCTGCTGC TGCCCCTGCT GCTGTCGCTG CTGCTGTGGT TGGCGCCCGG GGCCTGGGGC	120

TGGACGCGGG	GCGCCCCCG	GCCGCCGCC	AGCAGCCCGC	CGCTCTCCAT	CATGGGCCTC	180
ATGCCGCTCA	CCAAGGAGGT	GGCCAAGGGC	AGCATCGGGC	GCGGCGTGCT	CCCCGCCGTG	240
GAGCTAGCCA	TCGAGCAGAT	CCGCAACGAG	TCACTCCTGC	GCCCCTACTT	CCTGGACCTG	300
CGACTCTATG	ACACCGAGTG	TGACAATGCA	AAGGGACTGA	AAGCCTTCTA	TGACGCAATA	360
AAGTATGGGC	CGAACCATTT	GATGGTGTTT	GGAGGCGTCT	GTCCGTCTGT	CACATCTATT	420
ATCGCGGAGT	CCCTCCAAGG	CTGGAATCTG	GTGCAGCTTT	CCTTCGCCGC	CACCACGCCT	480
GTTCTTGCGG	ATAAGAAGAA	GTACCCGTAT	TTCTTCCGGA	CGGTGCCGTC	AGACAACGCG	540
GTGAACCCCG	CCATCCTGAA	GCTCCTGAAG	CACTTCCGCT	GGCGGCGTGT	GGGCACACTC	600
ACGCAGGACG	TGCAGCGCTT	CTCCGAGGTG	AGGAATGACC	TGACTGGGGT	TCTGTATGGG	660
GAAGATATTG	AGATCTCAGA	CACAGAGAGT	TTCTCCAATG	ATCCCTGCAC	CAGCGTCAAA	720
AAGCTCAAGG	GGAATGACGT	GCGGATCATC	CTTGGCCAGT	TTGACCAGAA	TATGGCAGCA	780
AAAGTCTTCT	GTTGTGCCTT	CGAGGAGAGC	ATGTTTGGCA	GCAAGTACCA	GTGGATCATC	840
CCGGGATGGT	ACGAGCCTGC	GTGGTGGGAG	CAGGTGCATG	TGGAGGCCAA	TTCCTCACGC	900
TGCCTGCGCA	GAAGCCTCCT	GGCTGCCATG	GAAGGTTACA	TCGGAGTGGA	CTTTGAGCCC	960
CTGAGCTCCA	AACAAATCAA	GACCATCTCA	GGGAAGACTC	CACAGCAGTA	TGAAAGAGAG	1020
TACAACAGCA	AACGTTTCAAG	CGTGGGGCCC	AGCAAGTTCC	ATGGGTACGC	CTACGATGGG	1080
ATCTGGGTCA	TCGCCAAGAC	CCTACAGAGG	GCCATGGAGA	CACTGCATGC	CAGTAGCAGG	1140
CACCAGCGGA	TCCAGGACTT	CAACTACACA	GACCACACGC	TGGGCAAAAT	CATCCTCAAT	1200
GCCATGAACG	AGACCAACTT	CTTCGGGGTC	ACGGGTCAAG	TTGTGTTCCG	GAACGGGGAG	1260
AGAATGGGAA	CCATTAAATT	TACTCAATTT	CAAGACAGCA	GAGAGGTGAA	GGTCGGCGAA	1320
TACAACGCGG	TGGCTGACAC	ACTGGAGATC	ATCAATGACA	CCATAAGGTT	CCAGGGGTCC	1380
GAGCCACCCA	AGGACAAGAC	CATCATTCTG	GAGCAGCTTC	GGAAGATCTC	GCTTCCACTG	1440
TATAGCATCC	TGTCCGCTCT	CACCATCCTC	GGCATGATCA	TGGCCAGCGC	CTTCCTCTTC	1500
TTCAACATCA	AGAACCGGAA	CCAAAAGCTG	ATTAAGATGT	CAAGCCCCTA	CATGAACAAC	1560
CTCATCATCC	TGGGAGGAAT	GCTGTCCTAT	GCATCCATCT	TCCTCTTTGG	CCTCGATGGG	1620
TCCTTCGTCT	CAGAAAAGAC	CTTTGAAACA	CTCTGCACGG	TCCGGACCTG	GATTCTCACC	1680
GTGGGCTACA	CAACTGCCTT	TGGGGCCATG	TTTGCAAAGA	CCTGGAGGGT	CCATGCCATC	1740
TTCAAAAATG	TGAAGATGAA	GAAGAAGATC	ATCAAAGACC	AGAAGCTGCT	TGTGATTGTG	1800
GGGGGCATGC	TGCTCATCGA	CCTGTGCATC	CTGATCTGTT	GGCAGGCTGT	GGACCCCTG	1860
CGGAGGACAG	TAGAGAGGTA	CAGCATGGAG	CCGGACCCAG	CAGGCCGGGA	CATCTCCATC	1920
CGCCCATTGC	TGGAACACTG	CGAAAACACC	CACATGACCA	TCTGGCTTGG	CATTGTCTAC	1980
GCCTACAAGG	GGCTCCTCAT	GCTATTCGGT	TGTTTCTTGG	CATGGGAAAC	CCGCAATGTG	2040

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AGCATCCCTG CCCTCAACGA CAGCAAGTAC ATCGGCATGA GTGTGTACAA TGTGGGGATC      2100
ATGTGCATCA TCGGGGCTGC TGTCTCCTTC CTGACGCGTG ACCAGCCCAA CGTGCAGTTC      2160
TGCATCGTGG CCCTGGTCAT CATCTTCTGC AGCACCATCA CTCTCTGCCT GGTGTTTGTG      2220
CCAAAGCTCA TTA CTCTGAG GACAAACCCT GACGCAGCCCA CTCAGAACAG GCGGTTCCAG      2280
TTCACACAGA ACCAGAAGAA AGAAGATTCG AAGACCTCCA CTTCAGTCAC CAGCGTGAAC      2340
CAGGCGAGCA CGTCACGCCT GGAGGGACTG CAGTCAGAAA ACCACCGCCT TCGAATGAAG      2400
ATCACAGAGC TGGACAAAGA CTTGGAAGAA GTCACCATGC AGCTACAAGA CACACCAGAG      2460
AAGACCACAT ACATCAAACA GAATCACTAC CAAGAGCTCA ACGACATCCT CAGCTTGGGC      2520
AACTTCACAG AGAGCACAGA TGGAGGAAAG GCCATTCTAA AAAATCACCT CGATCAAAAC      2580
CCCCAGCTCC AGTGGAAACAC GACAGAGCCC TCAAGAACAT GCAAAGACCC CATAGAAGAC      2640
ATCAACTCCC CGGAGCACAT CCAGCGCCGG CTGTCGCTCC AGCTCCCCAT CCTTCACCAC      2700
GCCTACCTCC CATCCATCGG AGGCGTGGAT GCCAGCTGCG TCAGCCCCTG TGTCAGCCCT      2760
ACCGCCAGCC CTCGCCACAG ACACGTACCA CCCTCCTTCC GAGTCATGGT CTCGGGCCTG      2820
TAG                                                                    2823

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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 940 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Ala Ser Pro Pro Ser Ser Gly Gln Pro Arg Pro Pro Pro Pro Pro
1          5          10          15
Pro Pro Pro Ala Arg Leu Leu Leu Pro Leu Leu Leu Ser Leu Leu Leu
20        25        30
Trp Leu Ala Pro Gly Ala Trp Gly Trp Thr Arg Gly Ala Pro Arg Pro
35        40        45
Pro Pro Ser Ser Pro Pro Leu Ser Ile Met Gly Leu Met Pro Leu Thr
50        55        60
Lys Glu Val Ala Lys Gly Ser Ile Gly Arg Gly Val Leu Pro Ala Val
65        70        75        80
Glu Leu Ala Ile Glu Gln Ile Arg Asn Glu Ser Leu Leu Arg Pro Tyr
85        90        95

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Phe	Leu	Asp	Leu	Arg	Leu	Tyr	Asp	Thr	Glu	Cys	Asp	Asn	Ala	Lys	Gly	100	105	110
Leu	Lys	Ala	Phe	Tyr	Asp	Ala	Ile	Lys	Tyr	Gly	Pro	Asn	His	Leu	Met	115	120	125
Val	Phe	Gly	Gly	Val	Cys	Pro	Ser	Val	Thr	Ser	Ile	Ile	Ala	Glu	Ser	130	135	140
Leu	Gln	Gly	Trp	Asn	Leu	Val	Gln	Leu	Ser	Phe	Ala	Ala	Thr	Thr	Pro	145	150	155
Val	Leu	Ala	Asp	Lys	Lys	Lys	Tyr	Pro	Tyr	Phe	Phe	Arg	Thr	Val	Pro	165	170	175
Ser	Asp	Asn	Ala	Val	Asn	Pro	Ala	Ile	Leu	Lys	Leu	Leu	Lys	His	Phe	180	185	190
Arg	Trp	Arg	Arg	Val	Gly	Thr	Leu	Thr	Gln	Asp	Val	Gln	Arg	Phe	Ser	195	200	205
Glu	Val	Arg	Asn	Asp	Leu	Thr	Gly	Val	Leu	Tyr	Gly	Glu	Asp	Ile	Glu	210	215	220
Ile	Ser	Asp	Thr	Glu	Ser	Phe	Ser	Asn	Asp	Pro	Cys	Thr	Ser	Val	Lys	225	230	235
Lys	Leu	Lys	Gly	Asn	Asp	Val	Arg	Ile	Ile	Leu	Gly	Gln	Phe	Asp	Gln	245	250	255
Asn	Met	Ala	Ala	Lys	Val	Phe	Cys	Cys	Ala	Phe	Glu	Glu	Ser	Met	Phe	260	265	270
Gly	Ser	Lys	Tyr	Gln	Trp	Ile	Ile	Pro	Gly	Trp	Tyr	Glu	Pro	Ala	Trp	275	280	285
Trp	Glu	Gln	Val	His	Val	Glu	Ala	Asn	Ser	Ser	Arg	Cys	Leu	Arg	Arg	290	295	300
Ser	Leu	Leu	Ala	Ala	Met	Glu	Gly	Tyr	Ile	Gly	Val	Asp	Phe	Glu	Pro	305	310	315
Leu	Ser	Ser	Lys	Gln	Ile	Lys	Thr	Ile	Ser	Gly	Lys	Thr	Pro	Gln	Gln	325	330	335
Tyr	Glu	Arg	Glu	Tyr	Asn	Ser	Lys	Arg	Ser	Gly	Val	Gly	Pro	Ser	Lys	340	345	350
Phe	His	Gly	Tyr	Ala	Tyr	Asp	Gly	Ile	Trp	Val	Ile	Ala	Lys	Thr	Leu	355	360	365
Gln	Arg	Ala	Met	Glu	Thr	Leu	His	Ala	Ser	Ser	Arg	His	Gln	Arg	Ile	370	375	380
Gln	Asp	Phe	Asn	Tyr	Thr	Asp	His	Thr	Leu	Gly	Lys	Ile	Ile	Leu	Asn	385	390	395
Ala	Met	Asn	Glu	Thr	Asn	Phe	Phe	Gly	Val	Thr	Gly	Gln	Val	Val	Phe	405	410	415
Arg	Asn	Gly	Glu	Arg	Met	Gly	Thr	Ile	Lys	Phe	Thr	Gln	Phe	Gln	Asp	420	425	430

Ser	Arg	Glu	Val	Lys	Val	Gly	Glu	Tyr	Asn	Ala	Val	Ala	Asp	Thr	Leu
		435					440					445			
Glu	Ile	Ile	Asn	Asp	Thr	Ile	Arg	Phe	Gln	Gly	Ser	Glu	Pro	Pro	Lys
	450					455					460				
Asp	Lys	Thr	Ile	Ile	Leu	Glu	Gln	Leu	Arg	Lys	Ile	Ser	Leu	Pro	Leu
465					470					475					480
Tyr	Ser	Ile	Leu	Ser	Ala	Leu	Thr	Ile	Leu	Gly	Met	Ile	Met	Ala	Ser
				485					490					495	
Ala	Phe	Leu	Phe	Phe	Asn	Ile	Lys	Asn	Arg	Asn	Gln	Lys	Leu	Ile	Lys
			500					505					510		
Met	Ser	Ser	Pro	Tyr	Met	Asn	Asn	Leu	Ile	Ile	Leu	Gly	Gly	Met	Leu
		515					520					525			
Ser	Tyr	Ala	Ser	Ile	Phe	Leu	Phe	Gly	Leu	Asp	Gly	Ser	Phe	Val	Ser
	530					535					540				
Glu	Lys	Thr	Phe	Glu	Thr	Leu	Cys	Thr	Val	Arg	Thr	Trp	Ile	Leu	Thr
545					550					555					560
Val	Gly	Tyr	Thr	Thr	Ala	Phe	Gly	Ala	Met	Phe	Ala	Lys	Thr	Trp	Arg
				565					570					575	
Val	His	Ala	Ile	Phe	Lys	Asn	Val	Lys	Met	Lys	Lys	Lys	Ile	Ile	Lys
			580					585					590		
Asp	Gln	Lys	Leu	Leu	Val	Ile	Val	Gly	Gly	Met	Leu	Leu	Ile	Asp	Leu
		595					600					605			
Cys	Ile	Leu	Ile	Cys	Trp	Gln	Ala	Val	Asp	Pro	Leu	Arg	Arg	Thr	Val
	610					615					620				
Glu	Arg	Tyr	Ser	Met	Glu	Pro	Asp	Pro	Ala	Gly	Arg	Asp	Ile	Ser	Ile
625					630					635					640
Arg	Pro	Leu	Leu	Glu	His	Cys	Glu	Asn	Thr	His	Met	Thr	Ile	Trp	Leu
				645					650					655	
Gly	Ile	Val	Tyr	Ala	Tyr	Lys	Gly	Leu	Leu	Met	Leu	Phe	Gly	Cys	Phe
			660					665					670		
Leu	Ala	Trp	Glu	Thr	Arg	Asn	Val	Ser	Ile	Pro	Ala	Leu	Asn	Asp	Ser
		675					680					685			
Lys	Tyr	Ile	Gly	Met	Ser	Val	Tyr	Asn	Val	Gly	Ile	Met	Cys	Ile	Ile
	690					695					700				
Gly	Ala	Ala	Val	Ser	Phe	Leu	Thr	Arg	Asp	Gln	Pro	Asn	Val	Gln	Phe
705					710					715					720
Cys	Ile	Val	Ala	Leu	Val	Ile	Ile	Phe	Cys	Ser	Thr	Ile	Thr	Leu	Cys
				725					730					735	
Leu	Val	Phe	Val	Pro	Lys	Leu	Ile	Thr	Leu	Arg	Thr	Asn	Pro	Asp	Ala
			740					745					750		
Ala	Thr	Gln	Asn	Arg	Arg	Phe	Gln	Phe	Thr	Gln	Asn	Gln	Lys	Lys	Glu
		755					760					765			

Asp	Ser	Lys	Thr	Ser	Thr	Ser	Val	Thr	Ser	Val	Asn	Gln	Ala	Ser	Thr
770						775					780				
Ser	Arg	Leu	Glu	Gly	Leu	Gln	Ser	Glu	Asn	His	Arg	Leu	Arg	Met	Lys
785					790				795						800
Ile	Thr	Glu	Leu	Asp	Lys	Asp	Leu	Glu	Glu	Val	Thr	Met	Gln	Leu	Gln
				805					810					815	
Asp	Thr	Pro	Glu	Lys	Thr	Thr	Tyr	Ile	Lys	Gln	Asn	His	Tyr	Gln	Glu
			820					825					830		
Leu	Asn	Asp	Ile	Leu	Ser	Leu	Gly	Asn	Phe	Thr	Glu	Ser	Thr	Asp	Gly
		835					840					845			
Gly	Lys	Ala	Ile	Leu	Lys	Asn	His	Leu	Asp	Gln	Asn	Pro	Gln	Leu	Gln
	850					855					860				
Trp	Asn	Thr	Thr	Glu	Pro	Ser	Arg	Thr	Cys	Lys	Asp	Pro	Ile	Glu	Asp
865					870					875					880
Ile	Asn	Ser	Pro	Glu	His	Ile	Gln	Arg	Arg	Leu	Ser	Leu	Gln	Leu	Pro
				885					890					895	
Ile	Leu	His	His	Ala	Tyr	Leu	Pro	Ser	Ile	Gly	Gly	Val	Asp	Ala	Ser
			900					905					910		
Cys	Val	Ser	Pro	Cys	Val	Ser	Pro	Thr	Ala	Ser	Pro	Arg	His	Arg	His
		915					920					925			
Val	Pro	Pro	Ser	Phe	Arg	Val	Met	Val	Ser	Gly	Leu				
	930					935					940				

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGGATGCTT TCCTATGCTT CCATATTTCT CTTTGGCCTT GATGG

45

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAATGTGCAG TTCTGCATCG TGGCTCTGGT CATCATCTTC TGCAG

45

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTTCTAGGCC TGTACGGAAG TGTT

24

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTTGTGGTTT GTCCAACTC ATCAAT

26

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGATGAGT[†]G TCTACAACGT GGGG

24

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGCGTTGCTG CATCTGGGTT TGTTC

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCTCCCTAC CTCTCTACAG CATCCT

26

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAGGTCCTGA CGGTGCAAAG TGTTTC

26

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGACGCAAGA CGTTCAGAGG TTCTCT

26

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGTAGCCTTC CATGGCAGCA AGCAGA

26

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGAGAACCTC TGAACGTCTT GCGTCA

26

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCTCTGTTG TGTTCCACTG TAGCTG

26

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCATGCCGCT CACCAAGGAG GTGGCC

26

2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCCACCTCC TTGGTGAGCG GCATGA

26

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGAGTGAGCA GAGTCCAGAG CCGT

24

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATGGATGGGA GGTAGGCGTG GTGGAG

26

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTCTCTGCCC TCACCATCCT CGGGAT

26

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GACTCCGGCT CGAATACCAG GCAGAG

26

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCATGTTTGC AAAGACCTGG AGGGTCC

27

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGTCACGCGT CAGGAAAGAG ACAGCAG

27

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAGCTTCTAG AGATCCCTCG ACCTC

25

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AGGCGCAGAA CTGGTAGGTA TGGAA

25

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTTCTAGGCC TGTACGGAAG TGTTA

25

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTTGTGGTTT GTCCAACTC ATCAATG

27

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTGCTGTCTC TTTCTGACG CGTGACC

27

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCAAGCTTCT AATACGACTC ACTATAGGGG AGACCATGGG CCCGGGGGGA CCCTGTACC

59

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTCATT GTAAAGCAAA TGTACTCGAC

60

TCC

63

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGCGGATC~~CA~~ TTATGTCTGC ACTCCGAAGG AAATTTG

37

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGCGAATTCT TATGTGAAGC GATCAGAGTT CATTTTTC

38

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCGGGATCCG CTATGGCTGG TGATTCTAGG AATG

34

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCGGAATTCC CCTCACACCG AGCCCCTGG

29

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCAATAAAGT ATGGGCTGAA CCATTTGATG GTGTTTGGAG GCGT

44

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ACGCCTCCAA ACACCATCAA ATGGTTCAGC CCATACTTTA TTGC

44

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTGAGCCCC TGAGCTCCAA ACAAATCAAG ACCATCTCAG

40

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTGAGATGGT CTTGATTTGT TTGGAGCTCA GGGGCTCAAA

40

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AAGGCCATCA ACTTCCTGCC TGTGGACTAT GAGATCGAAT ATG

43

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CATATTCGAT CTCATAGTCC ACAGGCAGGA AGTTGATGGC CTT

43

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TGGCCGCTGC CTCTTCTGCT GGTGATGGCG GCTGGGGT

38

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACCCAGCCG CCATCACCAG CAGAAGAGGC AGCGGCCA

38

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCTTGGCTTT GGCCTTGAAC AAGACGTCTG GAGGAGGTGG TCGTT

45

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AACGACCACC TCCTCCAGAC GTCTTGTTCA AGGCCAAAGC CAAGG

45

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2826 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATGGCTTCCC CGCGGAGCTC CGGGCAGCCC GGGCCGCCGC CGCCGCCGCC ACCGCCGCC	60
GCGCGCCTGC TACTGCTACT GCTGCTGCCG CTGCTGCTGC CTCTGGCGCC CGGGGCCTGG	120
GGCTGGGCGC GGGGCGCCCC CCGGCCGCCG CCCAGCAGCC CGCCGCTCTC CATCATGGGC	180
CTCATGCCGC TCACCAAGGA GGTGGCCAAG GGCAGCATCG GGC GCGGTGT GCTCCCCGCC	240
GTGGA ACTGG CCATCGAGCA GATCCGCAAC GAGTCACTCC TGCGCCCCTA CTTCTCGAC	300
CTGCGGCTCT ATGACACGGA GTGCGACAAC GCAAAGGGT TGAAAGCCTT CTACGATGCG	360
ATAAAATACG GGCCGAACCA CTTGATGGTG TTTGGAGGCG TCTGTCCATC CGTCACATCC	420
ATCATTGCAG AGTCCCTCCA AGGCTGGAAT CTGGTG CAGC TTTCTTTTGC TGCAACCACG	480
CCTGTTCTAG CCGATAAGAA AAAATACCCT TATTTCTTTC GGACCGTCCC ATCAGACAAT	540
GCGGTGAATC CAGCCATTCT GAAGTTGCTC AAGCACTACC AGTGGAAGCG CGTGGGCACG	600

CTGACGCAAG	ACG TTCAGAG	GTTCTCTGAG	GTGCGGAATG	ACCTGACTGG	AGTTCTGTAT	660
GGCGAGGACA	TTGAGATTTT	AGACACCGAG	AGCTTCTCCA	ACGATCCCTG	TACCA GTGTC	720
AAAAAGCTGA	AGGGGAATGA	TGTGCGGATC	ATCCTTGGCC	AGTTTGACCA	GAATATGGCA	780
GCAAAAGTGT	TCTGTTGTGC	ATACGAGGAG	AACATGTATG	G TAGTAAATA	TCAGTGGATC	840
ATTCCGGGCT	GGTACGAGCC	TTCTTGGTGG	GAGCAGGTGC	ACACGGAAGC	CAACTCATCC	900
CGCTGCCTCC	GGAAGAATCT	GCTTGCTGCC	ATGGAGGGCT	ACATTGGCGT	GGATTTCGAG	960
CCCCTGAGCT	CCAAGCAGAT	CAAGACCATC	TCAGGAAAGA	CTCCACAGCA	GTATGAGAGA	1020
GAGTACAACA	ACAAGCGGTC	AGGCGTGGGG	CCCAGCAAGT	TCCACGGGTA	CGCCTACGAT	1080
GGCATCTGGG	TCATCGCCAA	GACACTGCAG	AGGGCCATGG	AGACACTGCA	TGCCAGCAGC	1140
CGGCACCAGC	GGATCCAGGA	CTTCAACTAC	ACGGACCACA	CGCTGGGCAG	GATCATCCTC	1200
AATGCCATGA	ACGAGACCAA	CTTCTTCGGG	GTCACGGGTC	AAGTTGTATT	CCGGAATGGG	1260
GAGAGAATGG	GGACCATTAA	ATTTACTCAA	TTTCAAGACA	GCAGGGAGGT	GAAGGTGGGA	1320
GAGTACAACG	CTGTGGCCGA	CACACTGGAG	ATCATCAATG	ACACCATCAG	GTTCCAAGGA	1380
TCCGAACCAC	CAAAAGACAA	GACCATCATC	CTGGAGCAGC	TGCGGAAGAT	CTCCCTACCT	1440
CTCTACAGCA	TCCTCTCTGC	CCTCACCATC	CTCGGGATGA	TCATGGCCAG	TGCTTTTCTC	1500
TTCTTCAACA	TCAAGAACCG	GAATCAGAAG	CTCATAAAGA	TGTCGAGTCC	ATACATGAAC	1560
AACCTTATCA	TCCTTGAGAG	GATGCTTTCC	TATGCTTCCA	TATTTCTCTT	TGGCCTTGAT	1620
GGATCCTTTG	TCTCTGAAAA	GACCTTTGAA	ACACTTTGCA	CCGTCAGGAC	CTGGATTCTC	1680
ACCGTGGGCT	ACACGACCGC	TTTTGGGGCC	ATGTTTGCAA	AGACCTGGAG	AGTCCACGCC	1740
ATCTTCAAAA	ATGTGAAAAT	GAAGAAGAAG	ATCATCAAGG	ACCAGAAACT	GCTTGTGATC	1800
GTGGGGGGCA	TGCTGCTGAT	CGACCTGTGT	ATCCTGATCT	GCTGGCAGGC	TGTGGACCCC	1860
CTGCGAAGGA	CAGTGGAGAA	GTACAGCATG	GAGCCGGACC	CAGCAGGACG	GGATATCTCC	1920
ATCCGCCCTC	TCCTGGAGCA	CTGTGAGAAC	ACCCATATGA	CCATCTGGCT	TGGCATCGTC	1980
TATGCCTACA	AGGGACTTCT	CATGTTGTTC	GGTTGTTTCT	TAGCTTGGGA	GACCCGCAAC	2040
GTCAGCATCC	CCGCACTCAA	CGACAGCAAG	TACATCGGGA	TGAGTGTCTA	CAACGTGGGG	2100
ATCATGTGCA	TCATCGGGGC	CGCTGTCTCC	TTCTTGACCC	GGGACCAGCC	CAATGTGCAG	2160
TTCTGCATCG	TGGCTCTGGT	CATCATCTTC	TGCAGCACCA	TCACCCTCTG	CCTGGTATTC	2220
GTGCCGAAGC	TCATCACCCCT	GAGAACAAAC	CCAGATGCAG	CAACGCAGAA	CAGGCGATTC	2280
CAGTTCACTC	AGAATCAGAA	GAAAGAAGAT	TCTAAAACGT	CCACCTCGGT	CACCAGTGTG	2340
AACCAAGCCA	GCACATCCCG	CCTGGAGGGC	CTACAGTCAG	AAAACCATCG	CCTGCGAATG	2400
AAGATCACAG	AGCTGGATAA	AGACTTGGAA	GAGGTCACCA	TGCAGCTGCA	GGACACACCA	2460
GAAAAGACCA	CCTACATTAA	ACAGAACCAC	TACCAAGAGC	TCAATGACAT	CCTCAACCTG	2520

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GGAAACTTCA CTGAGAGCAC AGATGGAGGA AAGGCCATTT TAAAAAATCA CCTCGATCAA      2580
AATCCCCAGC TACAGTGGAA CACAACAGAG CCCTCTCGAA CATGCAAAGA TCCTATAGAA      2640
GATATAAACT CTCCAGAACA CATCCAGCGT CGGCTGTCCC TCCAGCTCCC CATCCTCCAC      2700
CACGCCTACC TCCCATCCAT CGGAGGCGTG GACGCCAGCT GTGTCAGCCC CTGCGTCAGC      2760
CCCACCGCCA GCCCCCGCCA CAGACATGTG CCACCCTCCT TCCGAGTCAT GGTCTCGGGC      2820
CTGTAA                                           2826

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(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

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Met Ala Ser Pro Arg Ser Ser Gly Gln Pro Gly Pro Pro Pro Pro Pro
1           5           10           15
Pro Pro Pro Pro Ala Arg Leu Leu Leu Leu Leu Leu Leu Pro Leu Leu
20           25           30
Leu Pro Leu Ala Pro Gly Ala Trp Gly Trp Ala Arg Gly Ala Pro Arg
35           40           45
Pro Pro Pro Ser Ser Pro Pro Leu Ser Ile Met Gly Leu Met Pro Leu
50           55           60
Thr Lys Glu Val Ala Lys Gly Ser Ile Gly Arg Gly Val Leu Pro Ala
65           70           75           80
Val Glu Leu Ala Ile Glu Gln Ile Arg Asn Glu Ser Leu Leu Arg Pro
85           90           95
Tyr Phe Leu Asp Leu Arg Leu Tyr Asp Thr Glu Cys Asp Asn Ala Lys
100          105          110
Gly Leu Lys Ala Phe Tyr Asp Ala Ile Lys Tyr Gly Pro Asn His Leu
115          120          125
Met Val Phe Gly Gly Val Cys Pro Ser Val Thr Ser Ile Ile Ala Glu
130          135          140
Ser Leu Gln Gly Trp Asn Leu Val Gln Leu Ser Phe Ala Ala Thr Thr
145          150          155          160
Pro Val Leu Ala Asp Lys Lys Lys Tyr Pro Tyr Phe Phe Arg Thr Val
165          170          175
Pro Ser Asp Asn Ala Val Asn Pro Ala Ile Leu Lys Leu Leu Lys His

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	180	185	190
Tyr Gln Trp Lys Arg Val Gly Thr Leu Thr Gln Asp Val Gln Arg Phe	195	200	205
Ser Glu Val Arg Asn Asp Leu Thr Gly Val Leu Tyr Gly Glu Asp Ile	210	215	220
Glu Ile Ser Asp Thr Glu Ser Phe Ser Asn Asp Pro Cys Thr Ser Val	225	230	235
Lys Lys Leu Lys Gly Asn Asp Val Arg Ile Ile Leu Gly Gln Phe Asp	245	250	255
Gln Asn Met Ala Ala Lys Val Phe Cys Cys Ala Tyr Glu Glu Asn Met	260	265	270
Tyr Gly Ser Lys Tyr Gln Trp Ile Ile Pro Gly Trp Tyr Glu Pro Ser	275	280	285
Trp Trp Glu Gln Val His Thr Glu Ala Asn Ser Ser Arg Cys Leu Arg	290	295	300
Lys Asn Leu Leu Ala Ala Met Glu Gly Tyr Ile Gly Val Asp Phe Glu	305	310	315
Pro Leu Ser Ser Lys Gln Ile Lys Thr Ile Ser Gly Lys Thr Pro Gln	325	330	335
Gln Tyr Glu Arg Glu Tyr Asn Asn Lys Arg Ser Gly Val Gly Pro Ser	340	345	350
Lys Phe His Gly Tyr Ala Tyr Asp Gly Ile Trp Val Ile Ala Lys Thr	355	360	365
Leu Gln Arg Ala Met Glu Thr Leu His Ala Ser Ser Arg His Gln Arg	370	375	380
Ile Gln Asp Phe Asn Tyr Thr Asp His Thr Leu Gly Arg Ile Ile Leu	385	390	395
Asn Ala Met Asn Glu Thr Asn Phe Phe Gly Val Thr Gly Gln Val Val	405	410	415
Phe Arg Asn Gly Glu Arg Met Gly Thr Ile Lys Phe Thr Gln Phe Gln	420	425	430
Asp Ser Arg Glu Val Lys Val Gly Glu Tyr Asn Ala Val Ala Asp Thr	435	440	445
Leu Glu Ile Ile Asn Asp Thr Ile Arg Phe Gln Gly Ser Glu Pro Pro	450	455	460
Lys Asp Lys Thr Ile Ile Leu Glu Gln Leu Arg Lys Ile Ser Leu Pro	465	470	475
Leu Tyr Ser Ile Leu Ser Ala Leu Thr Ile Leu Gly Met Ile Met Ala	485	490	495
Ser Ala Phe Leu Phe Phe Asn Ile Lys Asn Arg Asn Gln Lys Leu Ile	500	505	510
Lys Met Ser Ser Pro Tyr Met Asn Asn Leu Ile Ile Leu Gly Gly Met			

	515		520		525
Leu	Ser Tyr Ala Ser Ile Phe	Leu Phe Gly Leu Asp	Gly Ser Phe Val		
530		535		540	
Ser Glu Lys Thr Phe Glu Thr Leu Cys Thr Val Arg Thr Trp Ile Leu		550		555	560
545					
Thr Val Gly Tyr Thr Thr Ala Phe Gly Ala Met Phe Ala Lys Thr Trp		565		570	575
Arg Val His Ala Ile Phe Lys Asn Val Lys Met Lys Lys Lys Ile Ile		580		585	590
Lys Asp Gln Lys Leu Leu Val Ile Val Gly Gly Met Leu Leu Ile Asp		595		600	605
Leu Cys Ile Leu Ile Cys Trp Gln Ala Val Asp Pro Leu Arg Arg Thr		610		615	620
Val Glu Lys Tyr Ser Met Glu Pro Asp Pro Ala Gly Arg Asp Ile Ser		625		630	635
625					640
Ile Arg Pro Leu Leu Glu His Cys Glu Asn Thr His Met Thr Ile Trp		645		650	655
Leu Gly Ile Val Tyr Ala Tyr Lys Gly Leu Leu Met Leu Phe Gly Cys		660		665	670
Phe Leu Ala Trp Glu Thr Arg Asn Val Ser Ile Pro Ala Leu Asn Asp		675		680	685
Ser Lys Tyr Ile Gly Met Ser Val Tyr Asn Val Gly Ile Met Cys Ile		690		695	700
Ile Gly Ala Ala Val Ser Phe Leu Thr Arg Asp Gln Pro Asn Val Gln		705		710	715
705					720
Phe Cys Ile Val Ala Leu Val Ile Ile Phe Cys Ser Thr Ile Thr Leu		725		730	735
Cys Leu Val Phe Val Pro Lys Leu Ile Thr Leu Arg Thr Asn Pro Asp		740		745	750
Ala Ala Thr Gln Asn Arg Arg Phe Gln Phe Thr Gln Asn Gln Lys Lys		755		760	765
Glu Asp Ser Lys Thr Ser Thr Ser Val Thr Ser Val Asn Gln Ala Ser		770		775	780
Thr Ser Arg Leu Glu Gly Leu Gln Ser Glu Asn His Arg Leu Arg Met		785		790	795
785					800
Lys Ile Thr Glu Leu Asp Lys Asp Leu Glu Glu Val Thr Met Gln Leu		805		810	815
Gln Asp Thr Pro Glu Lys Thr Thr Tyr Ile Lys Gln Asn His Tyr Gln		820		825	830
Glu Leu Asn Asp Ile Leu Asn Leu Gly Asn Phe Thr Glu Ser Thr Asp		835		840	845
Gly Gly Lys Ala Ile Leu Lys Asn His Leu Asp Gln Asn Pro Gln Leu					

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(iii) HYPOTHETICAL: NO

Pro Leu Tyr Ser Ile Leu Ser Ala Leu Thr Ile Leu Gly Met Ile Met
1 5 10 15
Ala Ser Ala Phe Leu Phe Phe Asn Ile Lys Asn
20 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(iii) HYPOTHETICAL: NO

Leu Ile Ile Leu Gly Gly Met Leu Ser Tyr Ala Ser Ile Phe Leu Phe
1 5 10 15

Gly Leu Asp Gly Ser Phe Val Ser Glu Lys Thr
20 25

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Cys	Thr	Val	Arg	Thr	Trp	Ile	Leu	Thr	Val	Gly	Tyr	Thr	Thr	Ala	Phe
1				5					10					15	
Gly	Ala	Met	Phe	Ala	Lys	Thr	Trp	Arg							
			20					25							

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Gln	Lys	Leu	Leu	Val	Ile	Val	Gly	Gly	Met	Leu	Leu	Ile	Asp	Leu	Cys
1				5					10					15	
Ile	Leu	Ile	Cys	Trp	Gln										
			20												

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met	Thr	Ile	Trp	Leu	Gly	Ile	Val	Tyr	Ala	Tyr	Lys	Gly	Leu	Leu	Met
1				5					10				15		

Leu Phe Gly Cys Phe Leu Ala Trp
20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Ala	Leu	Asn	Asp	Ser	Lys	Tyr	Ile	Gly	Met	Ser	Val	Tyr	Asn	Val	Gly
1				5				10						15	
Ile	Met	Cys	Ile	Ile	Gly	Ala	Ala	Val							
			20					25							

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Cys	Ile	Val	Ala	Leu	Val	Ile	Ile	Phe	Cys	Ser	Thr	Ile	Thr	Leu	Cys
1				5				10						15	
Leu	Val	Phe	Val	Pro	Lys	Leu	Ile	Thr	Leu	Arg	Thr	Asn			
			20					25							

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 844 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met	Gly	Pro	Gly	Gly	Pro	Cys	Thr	Pro	Val	Gly	Trp	Pro	Leu	Pro	Leu	1	5	10	15
Leu	Leu	Val	Met	Ala	Ala	Gly	Val	Ala	Pro	Val	Trp	Ala	Ser	His	Ser	20	25	30	
Pro	His	Leu	Pro	Arg	Pro	His	Pro	Arg	Val	Pro	Pro	His	Pro	Ser	Ser	35	40	45	
Glu	Arg	Arg	Ala	Val	Tyr	Ile	Gly	Ala	Leu	Phe	Pro	Met	Ser	Gly	Gly	50	55	60	
Trp	Pro	Gly	Gly	Gln	Ala	Cys	Gln	Pro	Ala	Val	Glu	Met	Ala	Leu	Glu	65	70	75	80
Asp	Val	Asn	Ser	Arg	Arg	Asp	Ile	Leu	Pro	Asp	Tyr	Glu	Leu	Lys	Leu	85	90	95	
Ile	His	His	Asp	Ser	Lys	Cys	Asp	Pro	Gly	Gln	Ala	Thr	Lys	Tyr	Leu	100	105	110	
Tyr	Glu	Leu	Leu	Tyr	Asn	Asp	Pro	Ile	Lys	Ile	Ile	Leu	Met	Pro	Gly	115	120	125	
Cys	Ser	Ser	Val	Ser	Thr	Leu	Val	Ala	Glu	Ala	Ala	Arg	Met	Trp	Asn	130	135	140	
Leu	Ile	Val	Leu	Ser	Tyr	Gly	Ser	Ser	Ser	Pro	Ala	Leu	Ser	Asn	Arg	145	150	155	160
Gln	Arg	Phe	Pro	Thr	Phe	Phe	Arg	Thr	His	Pro	Ser	Ala	Thr	Leu	His	165	170		175
Asn	Pro	Thr	Arg	Val	Lys	Leu	Phe	Glu	Lys	Trp	Gly	Trp	Lys	Lys	Ile	180	185	190	
Ala	Thr	Ile	Gln	Gln	Thr	Thr	Glu	Val	Phe	Thr	Ser	Thr	Leu	Asp	Asp	195	200	205	
Leu	Glu	Glu	Arg	Val	Lys	Glu	Ala	Gly	Ile	Glu	Ile	Thr	Phe	Arg	Gln	210	215	220	
Ser	Phe	Phe	Ser	Asp	Pro	Ala	Val	Pro	Val	Lys	Asn	Leu	Lys	Arg	Gln	225	230	235	240
Asp	Ala	Arg	Ile	Ile	Val	Gly	Leu	Phe	Tyr	Glu	Thr	Glu	Ala	Arg	Lys	245	250	255	
Val	Phe	Cys	Glu	Val	Tyr	Lys	Glu	Arg	Leu	Phe	Gly	Lys	Lys	Tyr	Val	260	265	270	
Trp	Phe	Leu	Ile	Gly	Trp	Tyr	Ala	Asp	Asn	Trp	Phe	Lys	Thr	Tyr	Asp	275	280	285	
Pro	Ser	Ile	Asn	Cys	Thr	Val	Glu	Glu	Met	Thr	Glu	Ala	Val	Glu	Gly	290	295	300	
His	Ile	Thr	Thr	Glu	Ile	Val	Met	Leu	Asn	Pro	Ala	Asn	Thr	Arg	Ser	305	310	315	320
Ile	Ser	Asn	Met	Thr	Ser	Gln	Glu	Phe	Val	Glu	Lys	Leu	Thr	Lys	Arg				

					325					330					335		
Leu	Lys	Arg	His	Pro	Glu	Glu	Thr	Gly	Gly	Phe	Gln	Glu	Ala	Pro	Leu		
			340					345					350				
Ala	Tyr	Asp	Ala	Ile	Trp	Ala	Leu	Ala	Leu	Ala	Leu	Asn	Lys	Thr	Ser		
		355					360					365					
Gly	Gly	Gly	Gly	Arg	Ser	Gly	Val	Arg	Leu	Glu	Asp	Phe	Asn	Tyr	Asn		
	370					375					380						
Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	Arg	Ala	Met	Asn	Ser	Ser	Ser		
385					390					395					400		
Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	Phe	Asp	Ala	Ser	Gly	Ser	Arg		
				405					410						415		
Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	Gln	Gly	Gly	Ser	Tyr	Lys	Lys		
			420					425					430				
Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	Asp	Leu	Ser	Trp	Ser	Lys	Thr		
		435					440					445					
Asp	Lys	Trp	Ile	Gly	Gly	Ser	Pro	Pro	Ala	Asp	Gln	Thr	Leu	Val	Ile		
	450					455					460						
Lys	Thr	Phe	Arg	Phe	Leu	Ser	Gln	Lys	Leu	Phe	Ile	Ser	Val	Ser	Val		
465					470					475					480		
Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	Val	Val	Cys	Leu	Ser	Phe	Asn		
				485					490						495		
Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	Gln	Asn	Ser	Gln	Pro	Asn	Leu		
		500						505					510				
Asn	Asn	Leu	Thr	Ala	Val	Gly	Cys	Ser	Leu	Ala	Leu	Ala	Ala	Val	Phe		
		515					520					525					
Pro	Leu	Gly	Leu	Asp	Gly	Tyr	His	Ile	Gly	Arg	Ser	Gln	Phe	Pro	Phe		
	530					535					540						
Val	Cys	Gln	Ala	Arg	Leu	Trp	Leu	Leu	Gly	Leu	Gly	Phe	Ser	Leu	Gly		
545					550				555						560		
Tyr	Gly	Ser	Met	Phe	Thr	Lys	Ile	Trp	Trp	Val	His	Thr	Val	Phe	Thr		
				565					570					575			
Lys	Lys	Glu	Glu	Lys	Lys	Glu	Trp	Arg	Lys	Thr	Leu	Glu	Pro	Trp	Lys		
				580				585					590				
Leu	Tyr	Ala	Thr	Val	Gly	Leu	Leu	Val	Gly	Met	Asp	Val	Leu	Thr	Leu		
		595				600						605					
Ala	Ile	Trp	Gln	Ile	Val	Asp	Pro	Leu	His	Arg	Thr	Ile	Glu	Thr	Phe		
						615					620						
Ala	Lys	Glu	Glu	Pro	Lys	Glu	Asp	Ile	Asp	Val	Ser	Ile	Leu	Pro	Gln		
625					630					635					640		
Leu	Glu	His	Cys	Ser	Ser	Lys	Lys	Met	Asn	Thr	Trp	Leu	Gly	Ile	Phe		
				645					650					655			
Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	Leu	Leu	Gly	Ile	Phe	Leu	Ala	Tyr		

	660		665		670
Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp His Arg Ala Val	675		680		685
Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro	690		695		700
Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala	705		710		715
Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe		725		730	735
Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu		740		745	750
Thr Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu		755		760	765
Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile		770		775	780
Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln		785		790	795
Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Asp		805		810	815
Pro Ser Gly Gly Leu Pro Arg Gly Pro Ser Glu Pro Pro Asp Arg Leu		820		825	830
Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys		835		840	